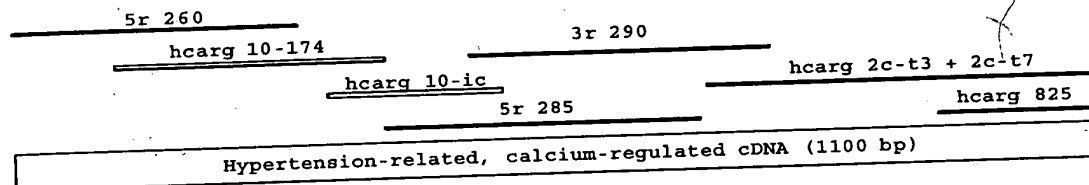


A



B

10904568-071601

Y
-131 SCACGAGCCACAGCCAGCTACCGCGGCTAGGTTCTCCAGGTGCAGAGGGCG -80
GTAAAGGCTTGTTGTATTGTAATGCAACTGTGGTTAGGACCTTCTCTTCGGACTGGTCAAGAAACGGGAAGAAAGG -1
ATG TCT GCT TTG GGG GCT GCA GCT CCA TAC TTG CAC CAT CCC GCT GAC AGT CAC AGT GGC 60
Met Ser Ala Leu Gly Ala Ala Pro Tyr Leu His His Pro Ala Asp Ser His Ser Gly
CGG GTC AGT TTC CTG GGT TCC CAG CCC TCT CCA GAA GTG ACG GCC GTG GCT CAG CTC TTG 120
Arg Val Ser Phe Leu Gly Ser Gln Pro Ser Pro Glu Val Thr Ala Val Ala Gln Leu Leu
AAG GAC TTA GAC AGG AGC ACC TTC AGA AAG TTG TTG AAA CTT GTA GTC GGG GCC CTG CAT 180
Lys Asp Leu Asp Arg Ser Thr Phe Arg Lys Leu Leu Lys Leu Val Val Gly Ala Leu His
GGG AAA GAC TGC AGA GAA GCT GTG GAG CAA CTT GGT GCC AGC GCC AAC CTG TCA GAA GAG 240
Gly Lys Asp Cys Arg Glu Ala Val Glu Gln Leu Gly Ala Ser Ala Asn Leu Ser Glu Glu
CGT CTG GCC GTC CTG CTG GCG GGC ACA CAC ACC CTG CTC CAG CAG GCT CTC CGG CTG CCC 300
Arg Leu Ala Val Leu Leu Ala Gly Thr His Thr Leu Leu Gln Gln Ala Leu Arg Leu Pro
CCT GCT AGT CTA AAG CCA GAT GCC TTC CAG GAA GAG CTC CAG GAA CTT GGC ATT CCT CAG 360
Pro Ala Ser Leu Lys Pro Asp Ala Phe Gln Glu Glu Leu Gln Glu Leu Gly Ile Pro Gln
GAT CTA ATT GGA GAT TTG GCC AGT TTG GCA TTT GGG AGT CAA CGC CCT CTT CTC GAC TCT 420
Asp Leu Ile Gly Asp Leu Ala Ser Leu Ala Phe Gly Ser Gln Arg Pro Leu Leu Asp Ser
GTA GCC CAA CAG CAG GGA TCC TCG CTG CCT CAC GTG TCT TAC TTC CGG TGG CGG GTG GAC 480
Val Ala Gln Gln Gln Gly Ser Ser Leu Pro His Val Ser Tyr Phe Arg Trp Arg Val Asp
GTG GCC ATC TCA ACC AGC GCT CAG TCC CGC TCC CTG CAA CCG AGT GTT CTC ATG CAG CTG 540
Val Ala Ile Ser Thr Ser Ala Gln Ser Arg Ser Leu Gln Pro Ser Val Leu Met Gln Leu
AAG CTC ACA GAT GGA TCT GCA CAC CGC TTC GAG GTG CCC ATA GCC AAA TTT CAG GAG CTG 600
Lys Leu Thr Asp Gly Ser Ala His Arg Phe Glu Val Pro Ile Ala Lys Phe Gln Glu Leu
CGG TAC AGT GTA GCC TTG GTC CTT AAG GAG ATG GCA GAA CTG GAG AAG AAG TGT GAG CGC 660
Arg Tyr Ser Val Ala Leu Val Leu Lys Glu Met Ala Glu Leu Lys Lys Cys Glu Arg
AAA CTG CAG GAC TGA CTGAACCCTGGTACTGTGGGTGCTGAAGCTGGTACCAGAACACAGCCCCCACTGGTGA 734
Lys Leu Gln Asp TER
TGAGCCCACTCCATTGAGGTCCCTGCATGTGAGAACGTATTTTAAAGTGAAAAGACAGCGGCACTTTCAGGTTTGTGTTT 813
ATGAGTCAACAGCTGGGCAGGGTGGCACAGTTTATAATCTCAGCCCTTGGAAGTCTGAGGCTGGAGAATGGGAAGTGTA 892
AGCTGGGCCTGGCTTTCATAGTGAGGCTCAGTGTGCAATTAAAGAGGTAAAGCAACTATTAAAAAAAAAAAAAAAAAAAA 969

FIGURE 1

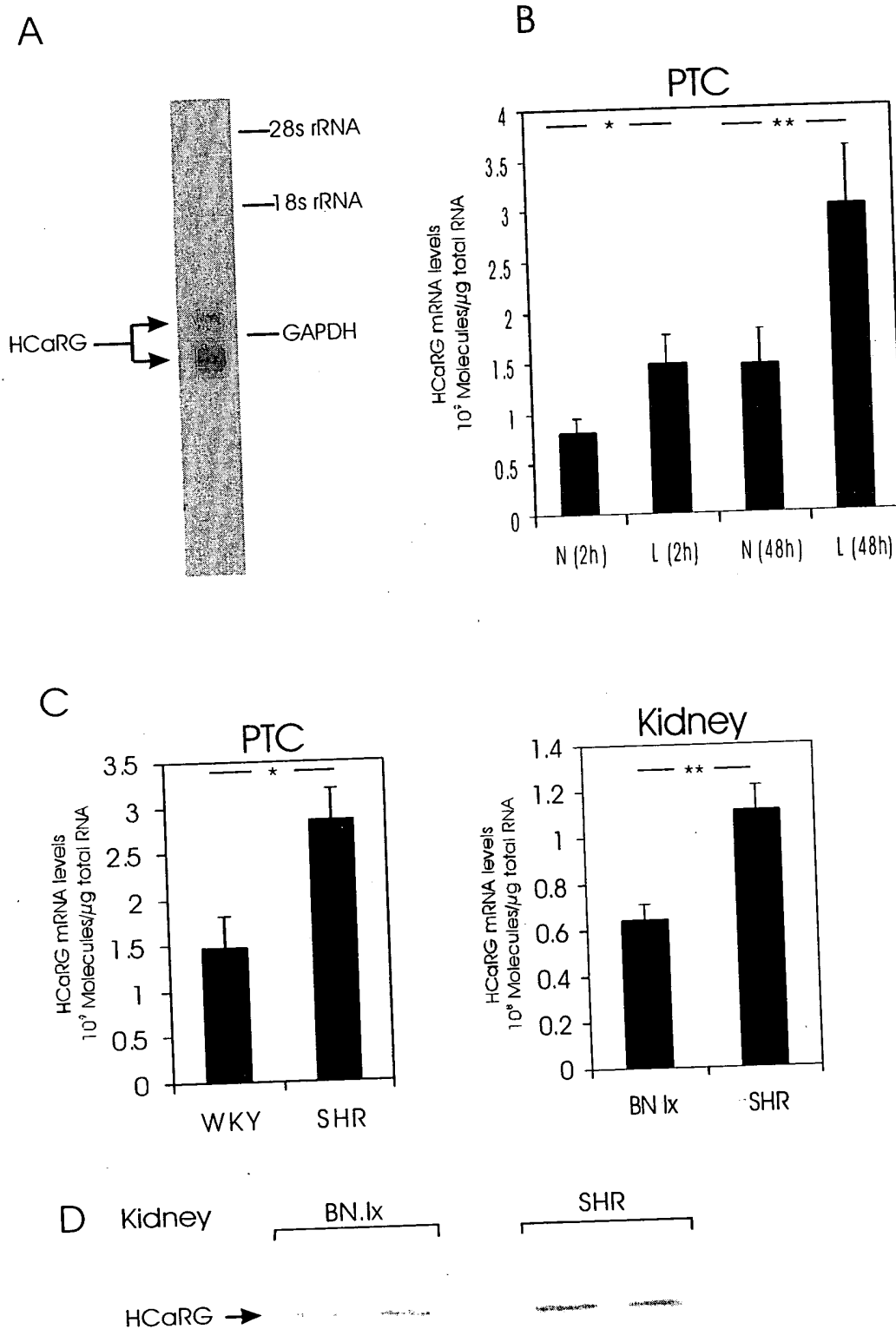


FIGURE 2

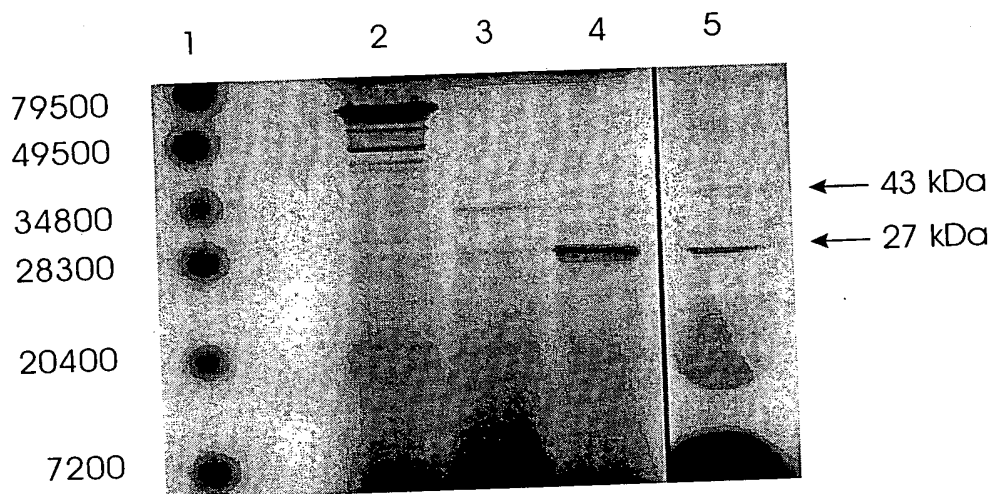


FIGURE 3

rHCaRG	MSA	GAA	PY	LHH	PAD	SHSG	RVS	FLG	SOPS	PEVT	AMA	QLL	KD	LD	RST	FRK	50
	MSA	VGA	TPY	LHH	PGD	SHSG	RVS	FLG	AQLP	PEVA	AMAR	LL	GD	LD	RST	FRK	50
rHCaRG	LLK	LVM	GALH	GKD	CREA	VEQ	LGAS	ANL	SEE	RLA	VLL	AGTH	TL	LQ	QAL	RRLP	100
	LLK	FVV	SSLQ	GED	CREA	VQR	LCVS	ANL	PEE	QL	GALL	AGMH	TL	LQ	QAL	RRLP	100
rHCaRG	PAS	LKP	DAFQ	EEL	QEL	CIPO	DLI	GDL	ASLA	FGS	QRPL	LDS	VA	QQ	QGS	SLP	150
	PT	SLK	PDI	ER	DQL	QEL	CIPO	DLV	GDL	ASVV	FGS	QRPL	LDS	VA	QQ	QCAWLP	150
rHCaRG	HVS	YFR	WRVD	VA	IST	SAQSR	SLO	PSV	LMQL	KI	TD	GSA	HRE	EV	ET	AKFOEL	200
	HVA	FR	WRVD	VA	IST	SALAR	SLO	PSV	LMQL	KI	SD	GSA	YRE	EV	ET	AKFOEL	200
rHCaRG	RYS	VAL	VLKE	MAE	LEK	KCER	KL	QD									224
	RYS	VAL	VLKE	MAD	LEK	RCER	RL	QD									224

FIGURE 4

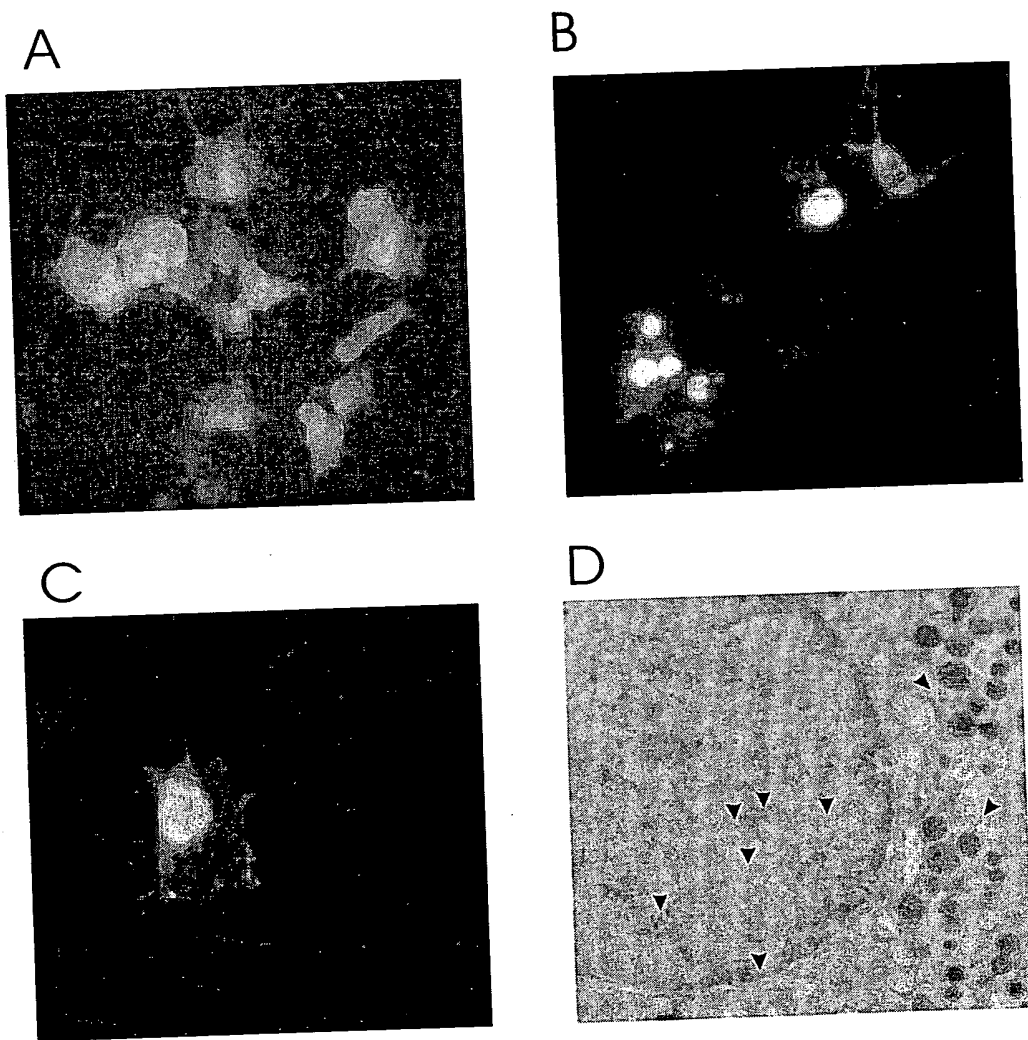
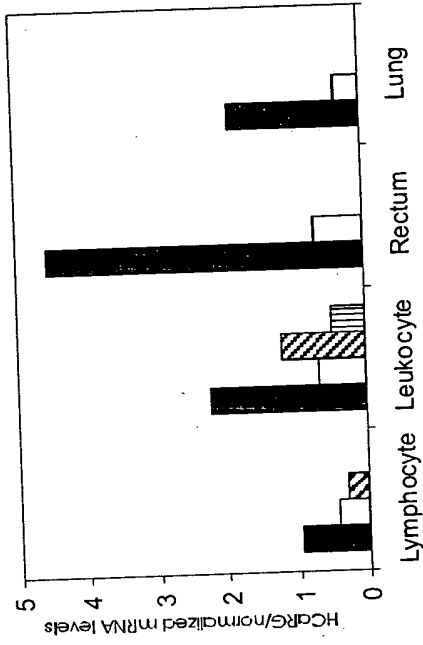
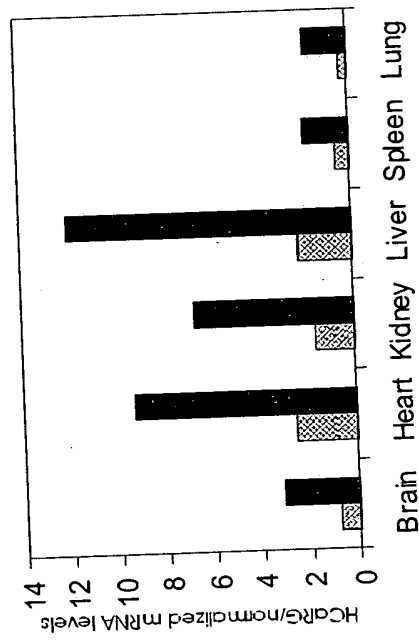


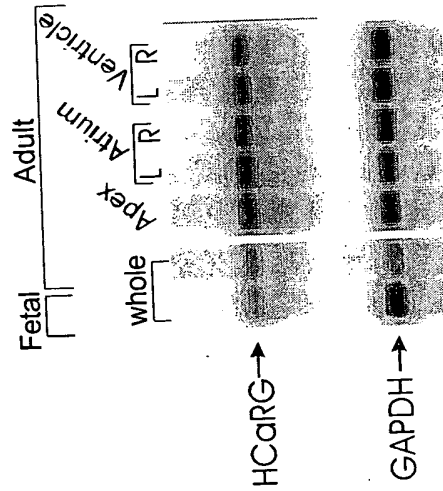
FIGURE 5

FIG 6: HCaRG mRNA expression in various tissues

A Fetal/Adult



B HEART



D Tumor/Normal

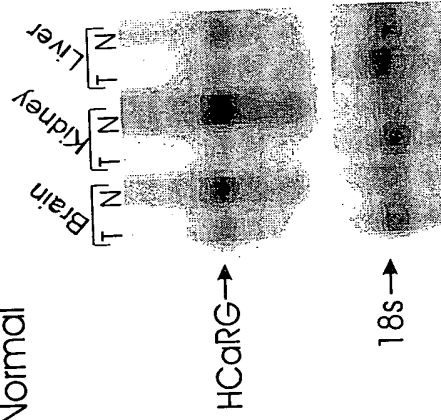


FIGURE 6

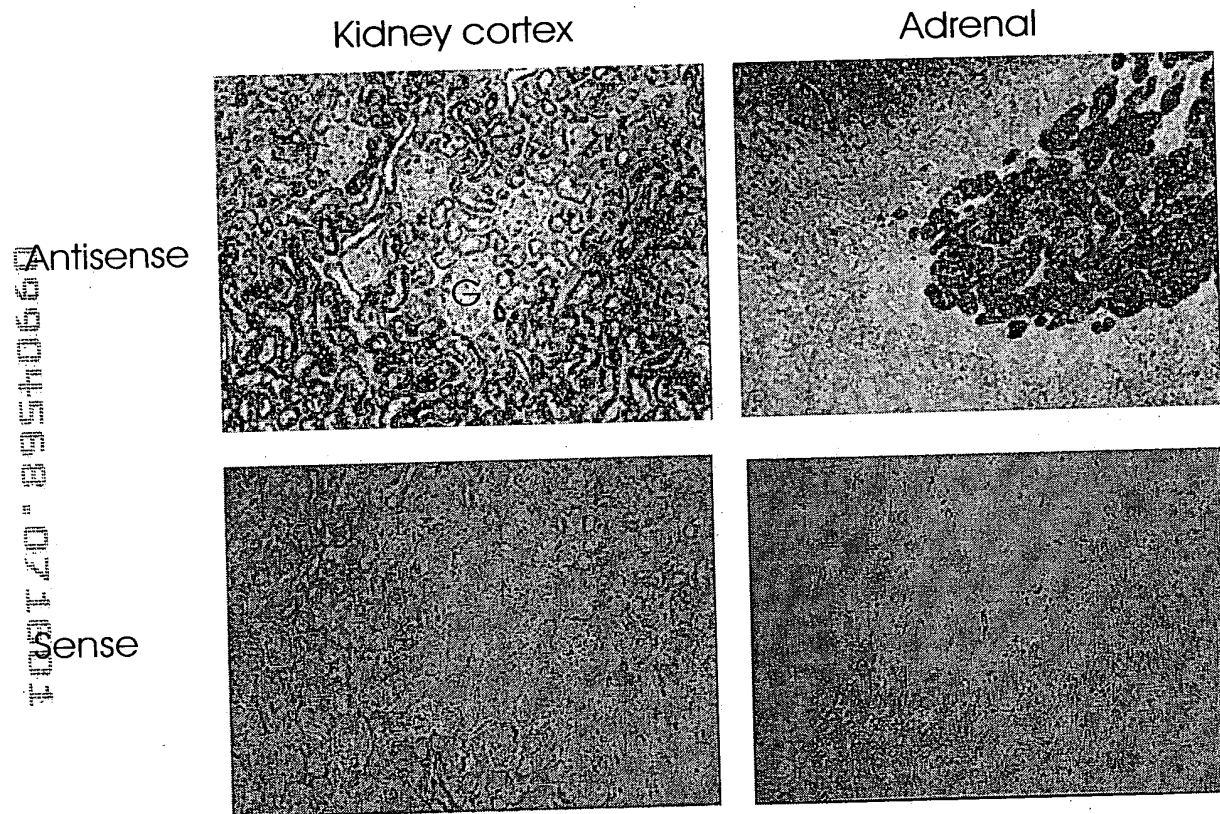
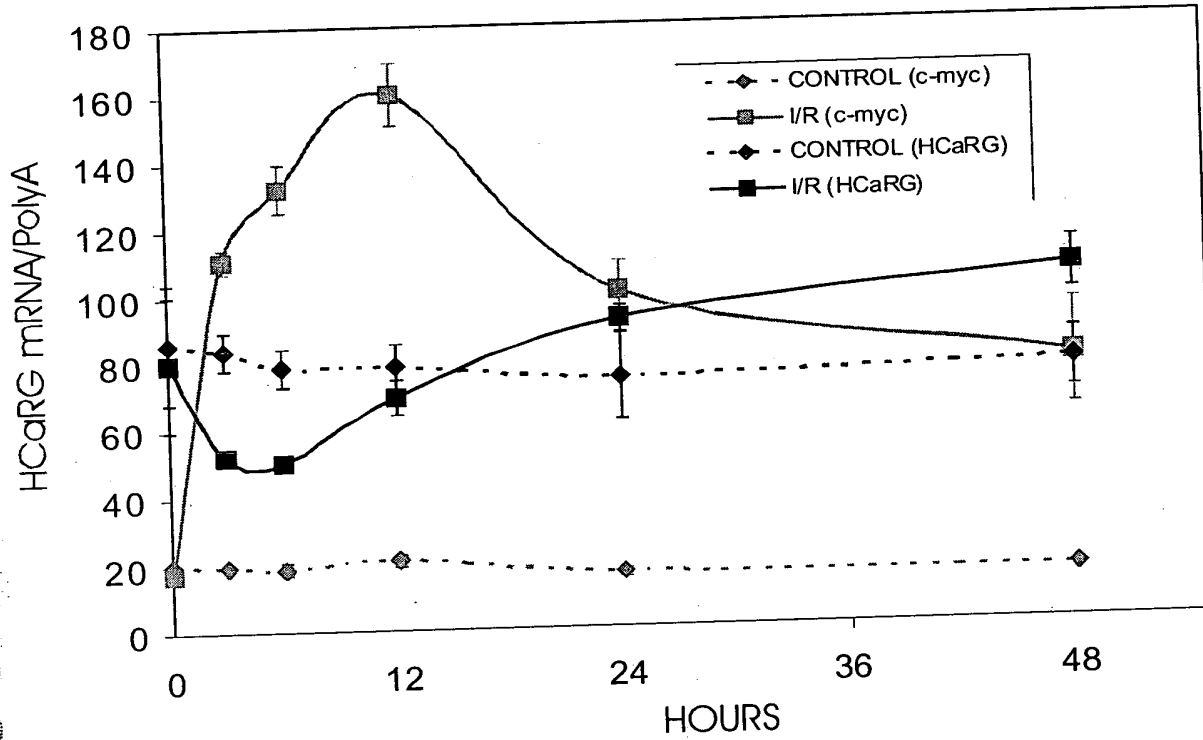
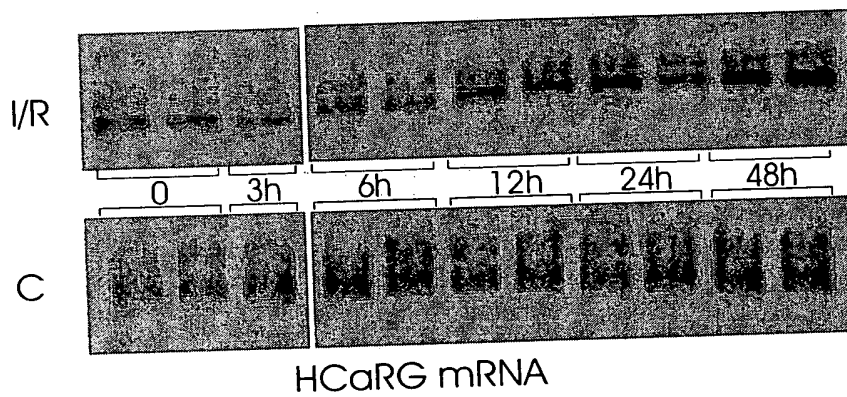


FIGURE 7

A Medulla



B Cortex



C Cortex

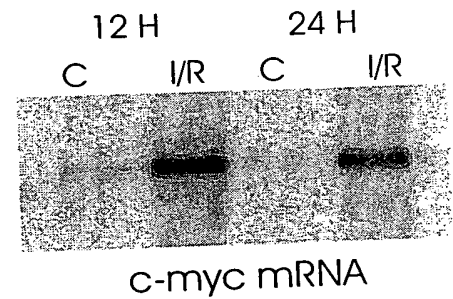
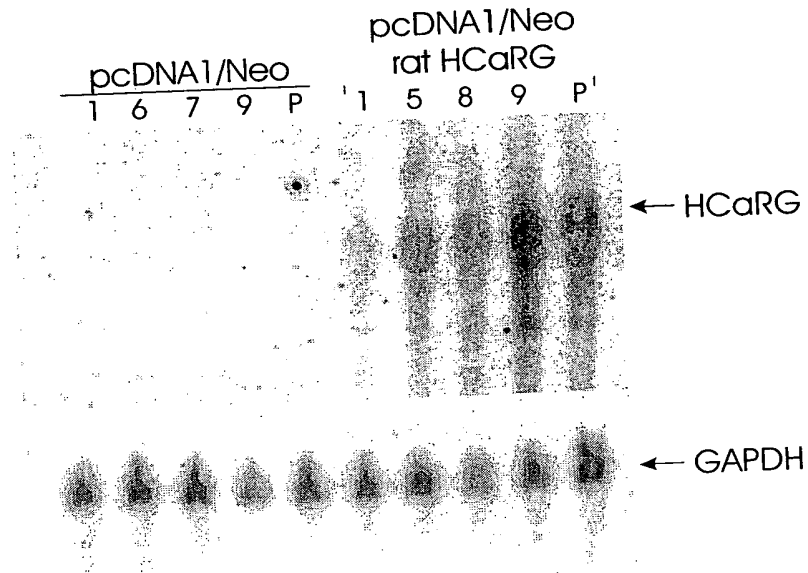


FIGURE 8

A

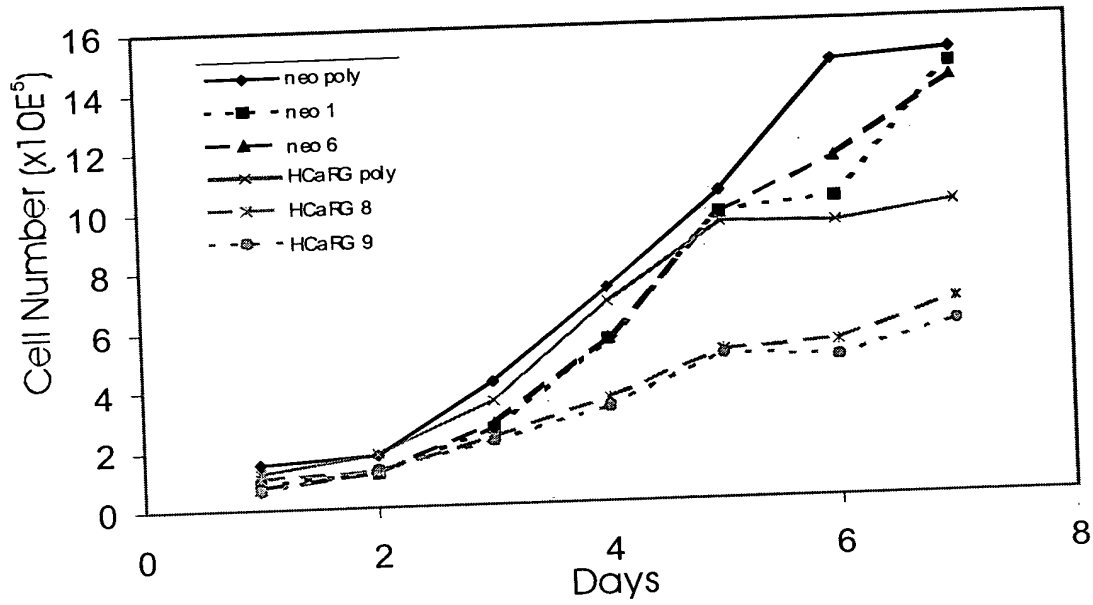


B



FIGURE 9

A



B

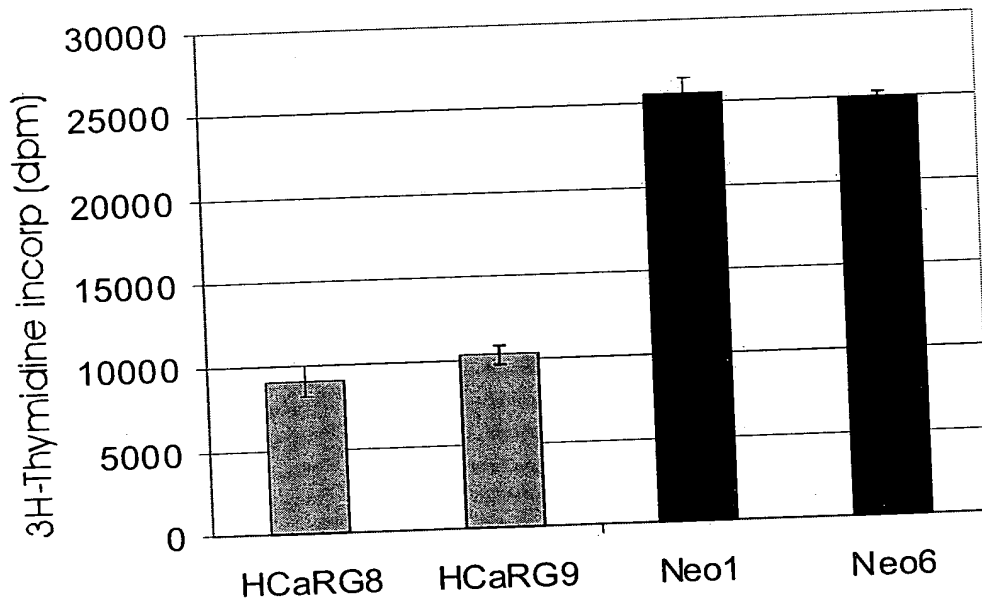


FIGURE 10

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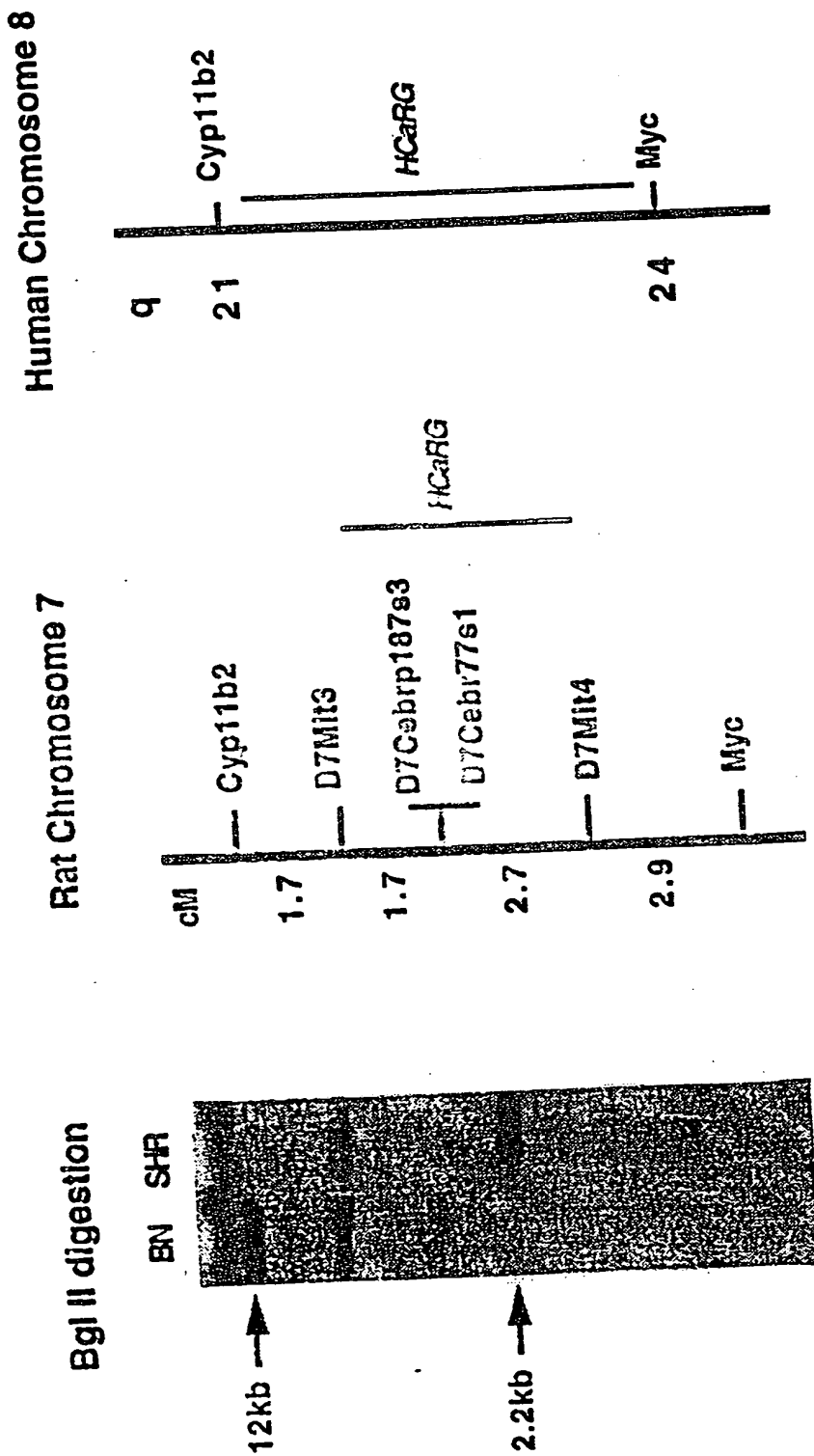


FIGURE 11